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Conference Abstract

Structuring Biological Survey Metadata for Reuse: Implementing the Humboldt Extension in Flemish Bird Monitoring Datasets on GBIF

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Abstract

The effective reuse of biodiversity data is essential for informing evidence-based policy. As the Global Biodiversity Information Facility (GBIF) increasingly aggregates data from diverse biological surveys, machine-readable metadata becomes progressively crucial. Structuring survey metadata from textual descriptions into standardized format improves their comparability and alignment with the FAIR (Findable, Accessible, Interoperable, Reusable) principles (Wilkinson et al. 2016). The Humboldt Extension for Ecological Inventories (TDWG Humboldt Extension Task Group 2024) provides a controlled vocabulary to capture key methodological details of surveys and monitoring, enabling more robust analyses of biodiversity indices across spatial and temporal scales.

At the Belgian Biodiversity Platform (BBPF), we apply the Humboldt Extension guidelines to enhance two bird monitoring datasets on GBIF. Although both represent counts of observed birds in Flemish areas, they differ in spatial scope and methodology: the Common Breeding bird monitoring in Flanders (Piesschaert et al. 2025) dataset, published by the Research Institute for Nature and Forest (INBO), uses point counts across 1x1 km squares throughout the entire Flemish region, while the Bird census counts at the Zwin Nature Park (Faveyts and Cooleman 2025) dataset, published by the BBPF, combines point and transect counts within one location.

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In this presentation, we review our practices for selecting and mapping Humboldt Extension terms in both sampling-event datasets. We thereby highlight our findings on how to structure their events' metadata hierarchically to reflect spatial nesting, sampling effort, and taxonomic scope. For instance, both protocols focus on the same target taxonomic scope at the class' rank (Aves). A critical distinction, however, is that only the Common Breeding bird monitoring protocol excludes certain behavior-based observations of species groups breeding outside the counting area, such as foraging gulls (Larinae) and herons (Ardeinae) or corvids (Corvidae) in flocks flying over. Consequently, the *excludedTaxonomicScope* term is technically appropriate for mapping that methodological difference. Generically, we propose a schema that facilitates the identification of protocol-specific nuances and supports the more accurate derivation of species densities, abundances, and absences.

Implementing the Humboldt Extension to Darwin Core in these real-world cases demonstrates the practical value of structured metadata for enhancing biodiversity data interoperability and reusability. This standardization generally contributes to meeting targets of the Global Biodiversity Framework.

Keywords

ecological inventories, data mapping, interoperable, science support

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Conflicts of interest

The authors have declared that no competing interests exist.

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